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       Pastorek, Jaromir

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ccc gga gag gag gat cta cct gga gag gag gat cta cct gga gag gag    291
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tta gag gat cta cct act gtt gag gct cct gga gat cct caa gaa ccc    387
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aat ggg cga gtg att gag gcc tcc ttc cct gct gga gtg gac agc agt    1203
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10

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<212> PRT
<213> HUMAN

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            20   25   30

Met Pro Val His Pro
        35

<210> 7
<211> 25
<212> DNA
<213> HUMAN

<400> 7
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<210> 8
<211> 26
<212> DNA
<213> HUMAN
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11

<400> 8
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<210> 9
<211> 48
<212> DNA
<213> HUMAN

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<221> primer_bind
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<223> anchor primer that anneals to the homopolymeric tail.

<220>
<221> inosine
<222> (36)..(37) (41)..(42) (46)..(47)
<223> each of the modified_bases at positions (36), (37), (41), (42), (46)
and (47) are inosine

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cuacuacuac uaggccacgc gtcgactagt acgggaaggg aagggaag           48


<210> 10
<211> 6
<212> PRT
<213> HUMAN

<400> 10
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<210> 11
<211> 6
<212> PRT
<213> HUMAN

<400> 11
Gly Glu Asp Asp Pro Leu
  1               5


<210> 12
<211> 21

<212> PRT
<213> HUMAN

<400> 12
Asn Asn Ala His Arg Asp Lys Glu Gly Asp Asp Gln Ser His Trp Arg
1               5               10              15

Tyr Gly Gly Asp Pro
            20

<210> 13
<211> 16
<212> PRT
<213> HUMAN

<400> 13
His Pro Gln Arg Leu Pro Arg Met Gln Glu Asp Ser Pro Leu Gly Gly
1               5               10              15

<210> 14
<211> 24
<212> PRT
<213> HUMAN

<400> 14
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1               5               10              15

Pro Gly Glu Glu Asp Leu Pro Gly
            20

<210> 15
<211> 13
<212> PRT
<213> HUMAN

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Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala Tyr Glu Gln
1               5               10

<210> 16
<211> 16

<212> PRT
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<400> 20
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<210> 21


14

<400> 21
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<400> 22
Leu Glu His His His His His His
 1               5



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<300>
<301> Locker and Buzard,
<303> DNA Sequencing and Mapping
<304> 1
<306> 3-11
<307> 1990

<400> 24
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<210> 25
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<220>
<221> SITE
<222> (1)..(4)
<223> sequence element defined by Suzuki, J. Mol. Biol., 207:  61-84 (1989)
as motif frequently found in gene regulatory proteins.


<220>
<221> VARIANTS
<222> (3)..(4)
<223> variants in sequence element defined by Suzuki, J. Mol. Biol., 207:
61-84 (1989) as motif frequently found in gene regulatory proteins.

<400> 25
Ser Pro Xaa Xaa
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<210> 26
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<212> PRT
<213> HUMAN

<220>
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as a motif frequently found in gene regulatory proteins.

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<223> variants in sequence element defined by Suzuki, J. Mol. Biol., 207:
61-84 (1989) as a motif frequently found in gene regulatory proteins.

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1


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<211> 540
<212> DNA
<213> HUMAN

<220>
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<221> promoter
<222> (1)..(540)

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acatgagctg ctttccctct cagccagagg acatggggggg ccccagctcc cctgcctttc 180
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agctttggta tggggggagag ggcacagggc cagacaaacc tgtgagactt tggctccatc 420
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<210> 28
<211> 445
<212> DNA
<213> HUMAN

<220>
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<222> (1)
<223> 1st MN exon

<400> 28
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ctgtcactgc tgcttctggt gcctgtccat ccccagaggt tgccccggat gcaggaggat 180
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agtgaagagg attcacccag agaggaggat ccaccggag aggaggatct acctggagag 300
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aataatgccc acagggacaa agaag 445

<210> 29
<211> 30
<212> DNA
<213> HUMAN

<220>
<221> exon
<222> (1)
<223> 2nd MN exon

17

<400> 29
gggatgacca gagtcattgg cgctatggag

<210> 30
<211> 171
<212> DNA
<213> HUMAN

<220>
<221> exon
<222> (1)
<223> 3rd MN exon

<400> 30
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<210> 31
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<212> DNA
<213> HUMAN

<220>
<221> exon
<222> (1)
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<400> 31
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aaggccaccg tttccctgcc gag   143

<210> 32
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<212> DNA
<213> HUMAN

<220>
<221> exon
<222> (1)
<223> 5th MN exon

<400> 32
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<210> 33
<211> 67
<212> DNA
<213> HUMAN

<220>
<221> exon
<222> (1)
<223> 6th MN exon

<400> 33
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<210> 34
<211> 158
<212> DNA
<213> HUMAN

<220>
<221> exon
<222> (1)
<223> 7th MN exon

<400> 34
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gctacttcca atatgagggg tctctgacta caccgccctg tgcccagggt gtcatctgga 120
ctgtgtttaa ccagacagtg atgctgagtg ctaagcag   158

<210> 35
<211> 145
<212> DNA
<213> HUMAN

<220>
<221> exon
<222> (1)
<223> 8th MN exon

19

<400> 35
ctccacaccc tctctgacac cctgtgggga cctggtgact ctcggctaca gctgaacttc 60
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agcagtcctc gggctgctga gccag 145

<210> 36
<211> 27
<212> DNA
<213> HUMAN

<220>
<221> exon
<222> (1)
<223> 9th MN exon

<400> 36
cccagctgaa ttcctgcctg gctgctg   27

<210> 37
<211> 82
<212> DNA
<213> HUMAN

<220>
<221> exon
<222> (1)
<223> 10th MN exon

<400> 37
gtgacatcct agccctggtt tttggcctcc tttttgctgt caccagcgtc gcgttccttg 60
tgcagatgag aaggcagcac ag   82

<210> 38
<211> 191
<212> DNA
<213> HUMAN

<220>
<221> exon
<222> (1)
<223> 11th MN exon

<400> 38

20

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<213> HUMAN

<220>
<221> intron
<222> (1)..(1174)
<223> 1st MN intron

<400> 39
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<212> DNA
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<220>
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21

<222> (1)..(193)
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caccttttct acccgggttc cctaagttcc tgacctaggc gtcagacttc ctcactatac 180
tctcccaccc cag   193

<210> 41
<211> 131
<212> DNA
<213> HUMAN

<220>
<221> intron
<222> (1)..(131)
<223> 3rd MN intron

<400> 41
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tccctacgca g   131

<210> 42
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<212> DNA
<213> HUMAN

<220>
<221> intron
<222> (1)..(89)
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<400> 42
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<210> 43
<211> 1400
<212> DNA
<213> HUMAN

22

<220>
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<222> (1)..(1400)
<223> 5th MN intron

<400> 43
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<211> 1334
<212> DNA
<213> HUMAN

<220>
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<222> (1)..(1334)
<223> 6th MN intron

<400> 44
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gccagcgctc atcttgataa taaccatgaa gctgacagac acagttaccc gcaaacggct 180

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ggcctgcact tagtgaagaa gtggtctcag agttgagtta ccttggcttc tgggaggtga 1260
aactgtatcc ctataccctg aagctttaag ggggtgcaat gtagatgaga ccccaacata 1320
gatcctcttc acag                                                    1334


<210> 45
<211> 512
<212> DNA
<213> HUMAN

<220>
<221> intron
<222> (1)..(512)
<223> 7th MN intron

<400> 45
gtgggcctgg ggtgtgtgtg gacacagtgg gtgcggggga aagaggatgt aagatgagat 60
gagaaacagg agaagaaaga aatcaaggct gggctctgtg gcttacgcct ataatcccac 120
cacgttggga ggctgaggtg ggagaatggt ttgagcccag gagttcaaga caaggcgggg 180
caacatagtg tgaccccatc tctaccaaaa aaaccccaac aaaaccaaaa atagccgggc 240
atggtggtat gcggcctagt cccagctact caaggaggct gaggtgggaa gatcgcttga 300
ttccaggagt ttgagactgc agtgagctat gatcccacca ctgcctacca tctttaggat 360
acatttattt atttataaaa gaaatcaaga ggctggatgg ggaatacagg agctggaggg 420
tggagccctg aggtgctggt tgtgagctgg cctgggaccc ttgtttcctg tcatgccatg 480
aacccaccca cactgtccac tgacctccct ag                                512


<210> 46
<211> 114
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<212> DNA
<213> HUMAN

<220>
<221> intron
<222> (1)..(114)
<223> 8th MN intron

<400> 46
gtacagcttt gtctggtttc cccccagcca gtagtccctt atcctcccat gtgtgtgcca 60
gtgtctgtca ttggtggtca cagcccgcct ctcacatctc cttttctct ccag   114

<210> 47
<211> 617
<212> DNA
<213> HUMAN

<220>
<221> intron
<222> (1)..(617)
<223> 9th MN intron

<400> 47
gtgagtctgc ccctcctctt ggtcctgatg ccaggagact cctcagcacc attcagcccc 60
agggctgctc aggaccgcct ctgctccctc tccttttctg cagaacagac cccaacccca 120
atattagaga ggcagatcat ggtggggatt cccccattgt ccccagaggc taattgatta 180
gaatgaagct tgagaaatct cccagcatcc ctctcgcaaa agaatccccc cccctttttt 240
taaagatagg gtctcactct gtttgcccca ggctggggtg ttgtggcacg atcatagctc 300
actgcagcct cgaactccta ggctcaggca atcctttcac cttagcttct caaagcactg 360
ggactgtagg catgagccac tgtgcctggc cccaaacggc ccttttactt ggcttttagg 420
aagcaaaaac ggtgcttatc ttacccctc tcgtgtatcc accctcatcc cttggctggc 480
ctcttctgga gactgaggca ctatggggct gcctgagaac tcggggcagg ggtggtggag 540
tgcactgagg caggtgttga ggaactctgc agaccctct tccttcccaa agcagccctc 600
tctgctctcc atcgcag   617

<210> 48
<211> 130
<212> DNA
<213> HUMAN

<220>
<221> intron
<222> (1)..(130)
<223> 10th MN intron

<400> 48
gtattacact gaccctttct tcaggcacaa gcttccccca cccttgtgga gtcacttcat 60
gcaaagcgca tgcaaatgag ctgctcctgg ccagttttc tgattagcct ttcctgttgt 120
gtacacacag   130

<210> 49
<211> 1401
<212> DNA
<213> HUMAN

<400> 49
caaactttca cttttgttgc ccaggctgga gtgcaatggc gcgatctcgg ctcactgcaa 60
cctccacctc ccgggttcaa gtgattctcc tgcctcagcc tctagccaag tagctgcgat 120
tacaggcatg cgccaccacg cccggctaat ttttgtattt ttagtagaga cggggtttcg 180
ccatgttggt caggctggtc tcgaactcct gatctcaggt gatccaacca ccctggcctc 240
ccaaagtgct gggattatag gcgtgagcca gcgcctgg cctgaagcag ccactcactt 300
ttacagaccc taagacaatg attgcaagct ggtaggattg ctgtttggcc cacccagctg 360
cggtgttgag tttgggtgcg gtctcctgtg ctttgcacct ggcccgctta aggcatttgt 420
tacccgtaat gctcctgtaa ggcatctgcg tttgtgacat cgttttggtc gccaggaagg 480
gattggggct ctaagcttga gcggttcatc cttttcattt atacagggga tgaccagagt 540
cattggcgct atggaggtga gacacccacc cgctgcacag acccaatctg gaacccagc 600
tctgtggatc tcccctacag ccgtccctga acactggtcc cgggcgtccc acccgccgcc 660
caccgtccca ccccctcacc ttttctaccc gggttcccta agttcctgac ctaggcgtca 720
gacttcctca ctatactctc ccaccccagg cgacccgccc tggccccggg tgtccccagc 780
ctgcgcgggc cgcttccagt ccccggtgga tatccgcccc cagctcgccg ccttctgccc 840
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gcgcaacaat ggccacagtg gtgaggggg ctccccgccg agacttgggg atggggcggg 960
gcgcagggaa gggaaccgtc gcgcagtgcc tgcccggggg ttgggctggc cctaccgggc 1020
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atggctctgg gtcccgggcg ggagtaccgg gctctgcagc tgcatctgca ctggggggct 1140
gcaggtcgtc cgggctcgga gcacactgtg gaaggccacc gtttccctgc cgaggtgagc 1200
gcggactggc cgagaagggg caaaggagcg gggcggacgg gggccagaga cgtggccctc 1260
tcctaccctc gtgtcctttt cagatccacg tggttcacct cagcaccgcc tttgccagag 1320
ttgacgaggc cttggggcgc ccgggaggcc tggccgtgtt ggccgccttt ctggaggtac 1380
cagatcctgg acaccccta c   1401

<210> 50
<211> 59
<212> PRT
<213> HUMAN

<400> 50
Ser Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp Leu Pro Ser Glu
  1   5   10   15

Glu Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu Glu Asp Leu Pro
              20   25   30

Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Glu Val Lys Pro
              35   40   45

Lys Ser Glu Glu Glu Gly Ser Leu Lys Leu Glu
      50   55

<210> 51
<211> 257
<212> PRT
<213> HUMAN

<400> 51
Gly Asp Asp Gln Ser His Trp Arg Tyr Gly Gly Asp Pro Pro Trp Pro
  1   5   10   15

Arg Val Ser Pro Ala Cys Ala Gly Arg Phe Gln Ser Pro Val Asp Ile
              20   25   30

Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala Leu Arg Pro Leu Glu Leu
              35   40   45

Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu Leu Arg Leu Arg Asn Asn
      50   55   60

Gly His Ser Val Gln Leu Thr Leu Pro Pro Gly Leu Glu Met Ala Leu
 65   70   75   80

Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln Leu His Leu His Trp Gly
              85   90   95

Ala Ala Gly Arg Pro Gly Ser Glu His Thr Val Glu Gly His Arg Phe
              100   105   110

Pro Ala Glu Ile His Val Val His Leu Ser Thr Ala Phe Ala Arg Val
              115   120   125

Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu Ala Val Leu Ala Ala Phe
              130   135   140

Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala Tyr Glu Gln Leu Leu Ser
 145   150   155   160

27

Arg Leu Glu Glu Ile Ala Glu Glu Gly Ser Glu Thr Gln Val Pro Gly
                165   170   175

Leu Asp Ile Ser Ala Leu Leu Pro Ser Asp Phe Ser Arg Tyr Phe Gln
                180   185   190

Tyr Glu Gly Ser Leu Thr Thr Pro Pro Cys Ala Gln Gly Val Ile Trp
                195   200   205

Thr Val Phe Asn Gln Thr Val Met Leu Ser Ala Lys Gln Leu His Thr
        210   215   220

Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp Ser Arg Leu Gln Leu Asn
225   230   235   240

Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg Val Ile Glu Ala Ser Phe
                245   250   255

Pro

<210> 52
<211> 20
<212> PRT
<213> HUMAN

<400> 52
Ile Leu Ala Leu Val Phe Gly Leu Leu Phe Ala Val Thr Ser Val Ala
  1   5   10   15

Phe Leu Val Gln
            20

<210> 53
<211> 25
<212> PRT
<213> HUMAN

<400> 53
Met Arg Arg Gln His Arg Arg Gly Thr Lys Gly Gly Val Ser Tyr Arg
  1   5   10   15

Pro Ala Glu Val Ala Glu Thr Gly Ala
            20   25

28

<210> 54
<211> 59
<212> PRT
<213> HUMAN

<400> 54
Ser Ala Ser Glu Glu Pro Ser Pro Ser Glu Val Pro Phe Pro Ser Glu
 1   5   10   15

Glu Pro Ser Pro Ser Glu Glu Pro Phe Pro Ser Val Arg Pro Phe Pro
                20   25   30

Ser Val Val Leu Phe Pro Ser Glu Glu Pro Phe Pro Ser Lys Glu Pro
            35   40   45

Ser Pro Ser Glu Glu Pro Ser Ala Ser Glu Glu
        50   55

<210> 55
<211> 470
<212> RNA
<213> HUMAN

<400> 55
cauggccccg auaaccuucu gccugugcac acaccugccc cucacuccac ccccauccua 60
gcuuugguau gggggagagg gcacagggcc agacaaaccu gugagacuuu ggcuccaucu 120
cugcaaaagg gcgcucugug agucagccug cuccccucca ggcuugcucc uccccacccc 180
agcucucguu uccaaugcac guacagcccg uacacaccgu gugcugggac accccacagu 240
cagccgcaug gcuccccugu gccccagccc cuggcucccu cuguugaucc cggccccugc 300
uccaggccuc acugugcaac ugcugcuguc acugcugcuu cuggugccug uccaucccca 360
gagguugccc cggaugcagg aggauucccc cuugggagga ggcucuucug gggaagauga 420
cccacugggc gaggaggauc ugcccaguga agaggauuca cccagagagg   470

<210> 56
<211> 292
<212> DNA
<213> HUMAN

<400> 56
gttttttttga dacggagtct tgcatctgtc atgcccaggc tggagtagca gtggtgccat 60
ctcggctcac tgcaagctcc acctcccgag ttcacgccat tttcctgcct cagcctcccg 120
agtagctggg actacaggcg cccgccacca tgccggcta attttttgta ttttttggtag 180
agacggggtt tcaccgtgtt agccagaatg gtctcgatct cctgacttcg tgatccaccc 240

29

gcctcggcct cccaaagttc tgggattaca ggtgtgagcc accgcacctg gc   292

<210> 57
<211> 262
<212> DNA
<213> HUMAN

<400> 57
tttctttttt gagacagggt cttgctctgt cacccaggcc agagtgcaat ggtacagtct 60
cagctcactg cagcctcaac cgcctcggct caaaccatca tcccatttca gcctcctgag 120
tagctgggac tacaggcaca tgccattaca cctggctaat ttttttgtat ttctagtaga 180
gacagggttt ggccatgttg cccgggctgg tctcgaactc ctggactcaa gcaatccacc 240
cacctcagcc tcccaaaatg ag   262

<210> 58
<211> 2501
<212> DNA
<213> HUMAN

<220>
<221> misc_feature
<222> (1)..(2501)
<223> region 5' to transcription initiation site as determined by RNase
protection assay (nucleotide 3507 of Figures 2A-2F and of SEQ ID NO: 5),
corresponding to region of SEQ ID NO: 5 and Figures 2A-2F from nucleotide
(7) to nucleotide (2507), in which region some regulatory elements are
probably situated.

<220>
<221> unsure what base is at position 1968
<222> (1968)
<223> unsure of base at position 1968, which is the same unknown base as
that at position 1974 of SEQ ID NO. 5, i.e., the full-length MN genomic
sequence, and of that unknown at position 1968 of SEQ ID NO: 90, and
unknown at position 647 of SEQ ID NO: 110. That unknown base is in the 5'
region flanking the transcription initiation site (3507) as determined by
RNase protection assay.

<400> 58
tgttgactcg tgaccttacc cccaaccctg tgctctctga aacatgagct gtgtccactc 60
agggttaaat ggattaaggg cggtgcaaga tgtgctttgt taaacagatg cttgaaggca 120
gcatgctcgt taagagtcat caccaatccc taatctcaag taatcaggga cacaaacact 180
gcggaaggcc gcagggtcct ctgcctagga aaaccagaga cctttgttca cttgtttatc 240
tgaccttccc tccactattg tccatgaccc tgccaaatcc ccctctgtga gaaacaccca 300

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agaattatca ataaaaaaat aaatttaaaa aaaaaataca aaaaaaaaaa aaaaaaaaaa 360
aaaagactta cgaatagtta ttgataaatg aatagctatt ggtaaagcca agtaaatgat 420
catattcaaa accagacggc catcatcaca gctcaagtct acctgatttg atctctttat 480
cattgtcatt ctttggattc actagattag tcatcatcct caaaattctc ccccaagttc 540
taattacgtt ccaaacattt aggggttaca tgaagcttga acctactacc ttctttgctt 600
ttgagccatg agttgtagga atgatgagtt tacaccttac atgctgggga ttaatttaaa 660
ctttacctct aagtcagttg ggtagccttt ggcttatttt tgtagctaat tttgtagtta 720
atggatgcac tgtgaatctt gctatgatag ttttcctcca cactttgcca ctaggggtag 780
gtaggtactc agttttcagt aattgcttac ctaagaccct aagccctatt tctcttgtac 840
tggcctttat ctgtaatatg ggcatattta atacaatata attttttggag ttttttttgtt 900
tgtttgtttg tttgtttttt tgagacggag tcttgcatct gtcatgccca ggctggagta 960
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gtattttttgg tagagacggg gtttcaccgt gttagccaga atggtctcga tctcctgact 1140
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ctggccaatt ttttgagtct tttaaagtaa aaatatgtct tgtaagctgg taactatggt 1260
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atatctttta gcttcacttg gcttaaaagg ttctctcatt agcctaacac agtgtcattg 1440
ttggtaccac ttggatcata agtggaaaaa cagtcaagaa attgcacagt aatacttgtt 1500
tgtaagaggg atgattcagg tgaatctgac actaagaaac tcccctacct gaggtctgag 1560
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tgcatcaagt gagaacatat aatgtctgca tgtttccata tttcaggaat gtttgcttgt 1740
gtttatgct tttatataga cagggaaact tgttcctcag tgacccaaaa gaggtgggaa 1800
ttgttattgg atatcatcat tggcccacgc tttctgacct tggaaacaat taagggttca 1860
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ttggtaggaa ataagaatgt gaaactcttc agttggtgtg tgtccctngt tttttttgcaa 1980
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atcatgatct ttaaagatca ataatataat cctttcaagg attatgtctt tattataata 2100
aagataattt gtctttaaca gaatcaataa tataatccct taaaggatta tatctttgct 2160
gggcgcagtg gctcacacct gtaatcccag cactttgggt ggccaaggtg gaaggatcaa 2220
atttgcctac ttctatatta tcttctaaag cagaattcat ctctcttccc tcaatatgat 2280
gatattgaca gggtttgccc tcactcacta gattgtgagc tcctgctcag ggcaggtagc 2340
gttttttgtt tttgttttttg ttttttctttt ttgagacagg gtcttgctct gtcacccagg 2400
ccagagtgca atggtacagt ctcagctcac tgcagcctca accgcctcgg ctcaaaccat 2460
catcccattt cagcctcctg agtagctggg actacaggca c             2501
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<210> 59
<211> 292
<212> DNA
<213> HUMAN

<220>
<221> misc_feature

<222> (1)

<400> 59
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tcggctcact gcaagctcca cctcccgagt tcacgccatt ttcctgcctc agcctcccga 120
gtagctggga ctacaggcgc ccgccaccat gcccggctaa ttttttgtat ttttggtaga 180
gacggggttt caccgtgtta gccagaatgg tctcgatctc ctgacttcgt gatccacccg 240
cctcggcctc ccaaagttct gggattacag gtgtgagcca ccgcacctgg cc   292

<210> 60
<211> 262
<212> DNA
<213> HUMAN

<400> 60
ttctttttttg agacagggtc ttgctctgtc acccaggcca gagtgcaatg gtacagtctc 60
agctcactgc agcctcaacc gcctcggctc aaaccatcat cccatttcag cctcctgagt 120
agctgggact acaggcacat gccattacac ctggctaatt ttttgtatt tctagtagag 180
acagggtttg gccatgttgc ccgggctggt ctcgaactcc tggactcaag caatccaccc 240
acctcagcct cccaaaatga gg   262

<210> 61
<211> 294
<212> DNA
<213> HUMAN

<400> 61
ttttttttttg agacaaactt tcacttttgt tgcccaggct ggagtgcaat ggcgcgatct 60
cggctcactg caacctccac ctcccgggtt caagtgattc tcctgcctca gcctctagcc 120
aagtagctgc gattacaggc atgcgccacc acgcccggct aattttttgta tttttagtag 180
agacggggtt tcgccatgtt ggtcaggctg gtctcgaact cctgatctca ggtgatccaa 240
ccaccctggc ctcccaaagt gctgggatta taggcgtgag ccacagcgcc tggc   294

<210> 62
<211> 276
<212> DNA
<213> HUMAN

<400> 62
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tccgcctccc gggttcaagg gattctcctg cctcagcttc ctgagtagct ggggttacag 120
gtgtgtgcca ccatgcccag ctaattttt tttgtatttt tagtagacag gtttcacca 180
tgttggtcag gctggtctca aactcctggc ctcaagtgat ccgcctgact cagcctacca 240

32

aagtgctgat tacaagtgtg agccaccgtg cccagc   276

<210> 63
<211> 289
<212> DNA
<213> HUMAN

<400> 63
cgccgggcac ggtggctcac gcctgtaatc ccagcacttt gggaggccaa ggcaggtgga 60
tcacgaggtc aagagatcaa gaccatcctg gccaacatgg tgaaacccca tctctactaa 120
aaatacgaaa aaatagccag gcgtggtggc gggtgcctgt aatcccagct actcgggagg 180
ctgaggcagg agaatggcat gaacccggga ggcagaagtt gcagtgagcc gagatcgtgc 240
cactgcactc cagcctgggc aacagagcga gactcttgtc tcaaaaaaa   289

<210> 64
<211> 298
<212> DNA
<213> HUMAN

<400> 64
aggctgggct ctgtggctta cgcctataat cccaccacgt tgggaggctg aggtggggaga 60
atggtttgag cccaggagtt caagacaagg cggggcaaca tagtgtgacc ccatctctac 120
caaaaaaacc ccaacaaaac caaaaatagc cgggcatggt ggtatgcggc ctagtcccag 180
ctactcaagg aggctgaggt gggaagatcg cttgattcca ggagtttgag actgcagtga 240
gctatgatcc caccactgcc taccatcttt aggatacatt tatttattta taaaagaa   298

<210> 65
<211> 105
<212> DNA
<213> HUMAN

<400> 65
ttttttacat ctttagtaga gacagggttt caccatattg gccaggctgc tctcaaactc 60
ctgaccttgt gatccaccag cctcggcctc ccaaagtgct gggat   105

<210> 66
<211> 83
<212> DNA
<213> HUMAN

<400> 66
cctcgaactc ctaggctcag gcaatccttt caccttagct tctcaaagca ctgggactgt 60

aggcatgagc cactgtgcct ggc   83

<210> 67
<211> 11
<212> DNA
<213> HUMAN

<400> 67
agaaggtaag t   11

<210> 68
<211> 11
<212> DNA
<213> HUMAN

<400> 68
tggaggtgag a   11

<210> 69
<211> 11
<212> DNA
<213> HUMAN

<400> 69
cagtcgtgag g   11

<210> 70
<211> 11
<212> DNA
<213> HUMAN

<400> 70
ccgaggtgag c   11

<210> 71
<211> 11
<212> DNA
<213> HUMAN

<400> 71
tggaggtacc a   11

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<210> 72
<211> 11
<212> DNA
<213> HUMAN

<400> 72
ggaaggtcag t                                                    11


<210> 73
<211> 11
<212> DNA
<213> HUMAN

<400> 73
agcaggtggg c                                                    11


<210> 74
<211> 11
<212> DNA
<213> HUMAN

<400> 74
gccaggtaca g                                                    11


<210> 75
<211> 11
<212> DNA
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<400> 75
tgctggtgag t                                                    11


<210> 76
<211> 11
<212> DNA
<213> HUMAN

<400> 76
atacagggga t                                                    11
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<210> 77
<211> 11
<212> DNA
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<400> 77
atacagggga t   11

<210> 78
<211> 11
<212> DNA
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<400> 78
ccccaggcga c   11

<210> 79
<211> 11
<212> DNA
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<400> 79
acgcagtgca a   11

<210> 80
<211> 11
<212> DNA
<213> HUMAN

<400> 80
tttcagatcc a   11

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ccccaggagg g   11

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<211> 11
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tcacaggctc a   11

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<400> 83
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<400> 84
ctccagtcca g   11

<210> 85
<211> 12
<212> DNA
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<400> 85
tcgcaggtga ca   12

<210> 86
<211> 11
<212> DNA
<213> HUMAN

<400> 86
acacagaagg g   11

<210> 87
<211> 377

<212> PRT

<213> HUMAN

<400> 87

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Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp Leu Pro Ser Glu Glu
            20   25   30

Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu Glu Asp Leu Pro Gly
            35   40   45

Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Glu Val Lys Pro Lys
        50   55   60

Ser Glu Glu Glu Gly Ser Leu Lys Leu Glu Asp Leu Pro Thr Val Glu
65   70   75   80

Ala Pro Gly Asp Pro Gln Glu Pro Gln Asn Asn Ala His Arg Asp Lys
                85   90   95

Glu Gly Asp Asp Gln Ser His Trp Arg Tyr Gly Gly Asp Pro Pro Trp
            100   105   110

Pro Arg Val Ser Pro Ala Cys Ala Gly Arg Phe Gln Ser Pro Val Asp
        115   120   125

Ile Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala Leu Arg Pro Leu Glu
    130   135   140

Leu Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu Leu Arg Leu Arg Asn
145   150   155   160

Asn Gly His Ser Val Gln Leu Thr Leu Pro Pro Gly Leu Glu Met Ala
                165   170   175

Leu Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln Leu His Leu His Trp
            180   185   190

Gly Ala Ala Gly Arg Pro Gly Ser Glu His Thr Val Glu Gly His Arg
        195   200   205

Phe Pro Ala Glu Ile His Val Val His Leu Ser Thr Ala Phe Ala Arg
    210   215   220

38

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Val Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu Ala Val Leu Ala Ala
225             230             235             240

Phe Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala Tyr Glu Gln Leu Leu
            245             250             255

Ser Arg Leu Glu Glu Ile Ala Glu Glu Gly Ser Glu Thr Gln Val Pro
        260             265             270

Gly Leu Asp Ile Ser Ala Leu Leu Pro Ser Asp Phe Ser Arg Tyr Phe
        275             280             285

Gln Tyr Glu Gly Ser Leu Thr Thr Pro Pro Cys Ala Gln Gly Val Ile
    290             295             300

Trp Thr Val Phe Asn Gln Thr Val Met Leu Ser Ala Lys Gln Leu His
305             310             315             320

Thr Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp Ser Arg Leu Gln Leu
            325             330             335

Asn Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg Val Ile Glu Ala Ser
            340             345             350

Phe Pro Ala Gly Val Asp Ser Ser Pro Arg Ala Ala Glu Pro Val Gln
        355             360             365

Leu Asn Ser Cys Leu Ala Ala Gly Asp
    370             375
```

<210> 88
<211> 34
<212> DNA
<213> HUMAN

<400> 88
tagacagatc tacgatggct cccctgtgcc ccag   34

<210> 89
<211> 34
<212> DNA
<213> HUMAN

<400> 89

<210> 90
<211> 3532
<212> DNA
<213> HUMAN

<220>
<221> misc_feature which includes the MN gene promoter
<222> (1)..(3532)
<223> region including the transcription initiation site (nucleotide 3507
of SEQ ID NO: 5 and of Figures 2A-2F) as determined by RNase protection
assay, which region is inclusive of the MN gene promoter, and corresponds
to nucleotide 7 to nucleotide 3538 of SEQ ID NO: 5 and of Figures 2A-2F.

<220>
<221> unsure what base is at position 1968
<222> (1968)
<223> unsure of the base at position 1968, which is the same unknown base
at position 1974 of SEQ ID NO: 5 (the full-length MN genomic sequence),
position 1968 of SEQ ID NO: 58 and position 647 of SEQ ID NO: 110. That
unknown base is in the region that includes the transcription initiation
site (nucleotide 3507 of SEQ ID NO: 5 and of Figures 2A-2F) as determined
by RNase protection assay, which region is inclusive of the MN gene
promoter.

<400> 90
tgttgactcg tgaccttacc cccaaccctg tgctctctga aacatgagct gtgtccactc 60
agggttaaat ggattaaggg cggtgcaaga tgtgctttgt taaacagatg cttgaaggca 120
gcatgctcgt taagagtcat caccaatccc taatctcaag taatcaggga cacaaacact 180
gcggaaggcc gcagggtcct ctgcctagga aaaccagaga cctttgttca cttgtttatc 240
tgaccttccc tccactattg tccatgaccc tgccaaatcc ccctctgtga gaaacaccca 300
agaattatca ataaaaaaat aaatttaaaa aaaaaataca aaaaaaaaa aaaaaaaaa 360
aaaagactta cgaatagtta ttgataaatg aatagctatt ggtaaagcca agtaaatgat 420
catattcaaa accagacggc catcatcaca gctcaagtct acctgatttg atctctttat 480
cattgtcatt ctttggattc actagattag tcatcatcct caaaattctc ccccaagttc 540
taattacgtt ccaaacattt aggggttaca tgaagcttga acctactacc ttctttgctt 600
ttgagccatg agttgtagga atgatgagtt tacaccttac atgctgggga ttaatttaaa 660
ctttacctct aagtcagttg ggtagccttt ggcttatttt tgtagctaat tttgtagtta 720
atggatgcac tgtgaatctt gctatgatag ttttcctcca cactttgcca ctaggggtag 780
gtaggtactc agttttcagt aattgcttac ctaagaccct aagccctatt tctcttgtac 840
tggcctttat ctgtaatatg ggcatattta atacaatata atttttggag ttttttttgtt 900
tgtttgtttg tttgtttttt tgagacggag tcttgcatct gtcatgccca ggctggagta 960
gcagtggtgc catctcggct cactgcaagc tccacctccc gagttcacgc cattttcctg 1020
cctcagcctc ccgagtagct gggactacag gcgcccgcca ccatgcccgg ctaatttttt 1080

```
gtattttttgg  tagagacggg  gtttcaccgt  gttagccaga  atggtctcga  tctcctgact  1140
tcgtgatcca  cccgcctcgg  cctcccaaag  ttctgggatt  acaggtgtga  gccaccgcac  1200
ctggccaatt  ttttgagtct  tttaaagtaa  aaatatgtct  tgtaagctgg  taactatggt  1260
acatttcctt  ttattaatgt  ggtgctgacg  gtcatatagg  ttcttttgag  tttggcatgc  1320
atatgctact  ttttgcagtc  ctttcattac  attttttctct  cttcatttga  agagcatgtt  1380
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ttggtaccac  ttggatcata  agtggaaaaa  cagtcaagaa  attgcacagt  aatacttgtt  1500
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tttccttctt  actgtgttaa  aaaaaagtat  gatcttgctc  tgagaggtga  ggcattctta  2040
atcatgatct  ttaaagatca  ataatataat  cctttcaagg  attatgtctt  tattataata  2100
aagataattt  gtctttaaca  gaatcaataa  tataatccct  taaaggatta  tatctttgct  2160
gggcgcagtg  gctcacacct  gtaatcccag  cactttgggt  ggccaaggtg  gaaggatcaa  2220
atttgcctac  ttctatatta  tcttctaaag  cagaattcat  ctctcttccc  tcaatatgat  2280
gatattgaca  gggtttgccc  tcactcacta  gattgtgagc  tcctgctcag  ggcaggtagc  2340
gttttttgtt  tttgtttttg  tttttctttt  ttgagacagg  gtcttgctct  gtcacccagg  2400
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tcctggactc  aagcaatcca  cccacctcag  cctcccaaaa  tgagggaccg  tgtcttattc  2640
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aaaggtttgg  agaaaaaaat  aatagtttaa  tttggctaga  gtatgaggga  gagtagtagg  2820
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caatgtgcat  atcgtggcag  gcagtgggga  gccaatgaag  gcttttgagc  aggagagtaa  2940
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ccccgataac  cttctgcctg  tgcacacacc  tgccctcac   tccaccccca  tcctagcttt  3360
ggtatggggg  agagggcaca  gggccagaca  aacctgtgag  actttggctc  catctctgca  3420
aaagggcgct  ctgtgagtca  gcctgctccc  ctccaggctt  gctcctcccc  cacccagctc  3480
tcgtttccaa  tgcacgtaca  gcccgtacac  accgtgtgct  gggacacccc  ac          3532
```

<210> 91
<211> 204
<212> DNA

<213> HUMAN

<400> 91
cctgcccctc actccacccc catcctagct ttggtatggg ggagagggca cagggccaga 60
caaacctgtg agactttggc tccatctctg caaaagggcg ctctgtgagt cagcctgctc 120
ccctccaggc ttgctcctcc cccacccagc tctcgtttcc aatgcacgta cagcccgtac 180
acaccgtgtg ctgggacacc ccac 204

<210> 92
<211> 132
<212> DNA
<213> HUMAN

<400> 92
ggatcctgtt gactcgtgac cttaccccca accctgtgct ctctgaaaca tgagctgtgt 60
ccactcaggg ttaaatggat taagggcggt gcaagatgtg ctttgttaaa cagatgcttg 120
aaggcagcat gc 132

<210> 93
<211> 275
<212> DNA
<213> HUMAN

<400> 93
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ctgtgcacac acctgcccct cactccaccc ccatcctagc tttggtatgg gggagagggc 120
acagggccag acaaacctgt gagactttgg ctccatctct gcaaaagggc gctctgtgag 180
tcagcctgct cccctccagg cttgctcctc ccccacccag ctctcgtttc caatgcacgt 240
acagcccgta cacaccgtgt gctgggacac cccac 275

<210> 94
<211> 89
<212> DNA
<213> HUMAN

<400> 94
ctgctcccct ccaggcttgc tcctccccca cccagctctc gtttccaatg cacgtacagc 60
ccgtacacac cgtgtgctgg gacaccccca 89

<210> 95
<211> 61
<212> DNA

42

<213> HUMAN

<400> 95
cacccagctc tcgtttccaa tgcacgtaca gcccgtacac accgtgtgct gggacacccc 60
a   61

<210> 96
<211> 116
<212> DNA
<213> HUMAN

<400> 96
acctgcccct cactccaccc ccatcctagc tttggtatgg gggagagggc acagggccag 60
acaaacctgt gagactttgg ctccatctct gcaaaagggc gctctgtgag tcagcc   116

<210> 97
<211> 36
<212> PRT
<213> HUMAN

<400> 97
Gly Glu Glu Asp Leu Pro Ser Glu Glu Asp Ser Pro Arg Glu Glu Asp
1   5   10   15

Pro Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Gly Glu
            20   25   30

Glu Asp Leu Pro
        35

<210> 98
<211> 6
<212> PRT
<213> HUMAN

<400> 98
Gly Glu Glu Asp Leu Pro
  1   5

<210> 99
<211> 4
<212> PRT

43

<213> HUMAN

<400> 99
Glu Glu Asp Leu
  1

<210> 100
<211> 5
<212> PRT
<213> HUMAN

<400> 100
Glu Glu Asp Leu Pro
  1   5

<210> 101
<211> 6
<212> PRT
<213> HUMAN

<400> 101
Glu Asp Leu Pro Ser Glu
  1   5

<210> 102
<211> 7
<212> PRT
<213> HUMAN

<400> 102
Glu Glu Asp Leu Pro Ser Glu
  1   5

<210> 103
<211> 6
<212> PRT
<213> HUMAN

<400> 103
Asp Leu Pro Gly Glu Glu
  1   5

<210> 104
<211> 22
<212> PRT
<213> HUMAN

<400> 104
Gly Gly Ser Ser Gly Glu Asp Pro Leu Gly Glu Glu Asp Leu Pro
 1   5   10   15

Ser Glu Glu Asp Ser Pro
                20

<210> 105
<211> 25
<212> PRT
<213> HUMAN

<400> 105
Gly Glu Glu Asp Leu Pro Ser Glu Glu Asp Ser Pro Arg Glu Glu Asp
 1   5   10   15

Pro Pro Gly Glu Glu Asp Leu Pro Gly
                20   25

<210> 106
<211> 24
<212> PRT
<213> HUMAN

<400> 106
Glu Asp Pro Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro
 1   5   10   15

Gly Glu Glu Asp Leu Pro Glu Val
                20

<210> 107
<211> 7
<212> PRT
<213> HUMAN

<400> 107

Gly Glu Thr Arg Ala Pro Leu
    1   5

<210> 108
<211> 7
<212> PRT
<213> HUMAN

<400> 108
Gly Glu Thr Arg Glu Pro Leu
    1   5

<210> 109
<211> 7
<212> PRT
<213> HUMAN

<400> 109
Gly Gln Thr Arg Ser Pro Leu
    1   5

<210> 110
<211> 1247
<212> DNA
<213> HUMAN

<220>
<221> misc_feature
<222> (1)..(1247)
<223> region 5' to the transcription initiation site as determined by RNase
protection assay (nucleotide 3507 of SEQ ID NO: 5 and of Figures 2A-2F) in
which an activating element is localized, which region corresponds to
nucleotide 1328 to nucleotide 2574 of SEQ ID NO: 5 and of Figures 2A-2F.

<220>
<221> unsure what base is at position 647
<222> (647)
<223> unsure of the base at position 647, which is the same unknown base as
that at position 1974 of SEQ ID NO: 5, and as that at position 1968 of SEQ
ID NOS: 58 and 90. That unknown base at position 647 is in a region in
which an activating element is localized and is 5' to the transcription
initiation site.

<400> 110
```
tatgctactt tttgcagtcc tttcattaca ttttctctc ttcatttgaa gagcatgtta    60
tatcttttag cttcacttgg cttaaaaggt tctctcatta gcctaacaca gtgtcattgt   120
tggtaccact tggatcataa gtggaaaaac agtcaagaaa ttgcacagta atacttgttt   180
gtaagaggga tgattcaggt gaatctgaca ctaagaaact cccctacctg aggtctgaga   240
ttcctctgac attgctgtat ataggctttt cctttgacag cctgtgactg cggactattt   300
ttcttaagca agatatgcta aagttttgtg agccttttc cagagagagg tctcatatct    360
gcatcaagtg agaacatata atgtctgcat gtttccatat ttcaggaatg tttgcttgtg   420
ttttatgctt ttatatagac agggaaactt gttcctcagt gacccaaaag aggtgggaat   480
tgttattgga tatcatcatt ggcccacgct ttctgacctt ggaaacaatt aagggttcat   540
aatctcaatt ctgtcagaat tggtacaaga aatagctgct atgtttcttg acattccact   600
tggtaggaaa taagaatgtg aaactcttca gttggtgtgt gtccctngtt tttttgcaat   660
ttccttctta ctgtgttaaa aaaaagtatg atcttgctct gagaggtgag gcattcttaa   720
tcatgatctt taaagatcaa taatataatc ctttcaagga ttatgtcttt attataataa   780
agataatttg tctttaacag aatcaataat ataatccctt aaaggattat atctttgctg   840
ggcgcagtgg ctcacacctg taatcccagc actttgggtg gccaaggtgg aaggatcaaa   900
tttgcctact ctatattat cttctaaagc agaattcatc tctcttccct caatatgatg    960
atattgacag ggtttgccct cactcactag attgtgagct cctgctcagg gcaggtagcg   1020
tttttttgttt ttgttttttgt ttttctttt tgagacaggg tcttgctctg tcacccaggc   1080
cagagtgcaa tggtacagtc tcagctcact gcagcctcaa ccgcctcggc tcaaaccatc   1140
atcccatttc agcctcctga gtagctggga ctacaggcac atgccattac acctggctaa   1200
cttttttgta tttctagtag agacagggtt tggccatgtt gcccggg              1247
```

<210> 111
<211> 17
<212> DNA
<213> HUMAN

<400> 111
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ctctgtgagt cagcctg                                                    17
```

<210> 112
<211> 23
<212> DNA
<213> HUMAN

<400> 112
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aggcttgctc ctcccccacc cag                                             23
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<210> 113
<211> 18
<212> DNA
<213> HUMAN

<400> 113
agactttggc tccatctc   18

<210> 114
<211> 20
<212> DNA
<213> HUMAN

<400> 114
cactccaccc ccatcctagc   20

<210> 115
<211> 26
<212> DNA
<213> HUMAN

<400> 115
gggagagggc acagggccag acaaac   26

<210> 116
<211> 20
<212> PRT
<213> HUMAN

<400> 116
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 1   5   10   15

Gly Gly Gly Ser
            20